

SEQUENCE LISTING

<110> CHOI, YANG-DO
 CHEONG, JONG-JOO
 LEE, JONG-SEOB
 SONG, JONG-TAE
 SONG, SANG-IK
 SEO, HAK-SOO
 KOO, YEON-JONG

<120> GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID
 CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE
 DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS
 USING THE GENES

<130> 058333/0112

<140> 10/049,187

<141> 2002-02-08

<150> PCT/KR01/00953

<151> 2001-06-05

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1170

<212> DNA

<213> *Arabidopsis thaliana*

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<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (15)..(1181)

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Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile	
15 20 25	
ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg	146
Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met	
30 35 40	
atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc	194
Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys	
45 50 55 60	
tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg	242
Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr	
65 70 75	
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Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala	
95 100 105	
tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta	386
Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu	
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Gly Phe Gly Arg Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro	
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ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg	482
Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val	
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His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu	
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gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg	578
Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly	
175 180 185	

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 190 195 200

gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga tct 674
 Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser
 205 210 215 220

gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt aga 722
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 225 230 235

aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc 770
 Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu
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cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag gaa 818
 Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu
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 Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu
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ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag 962
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agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc 1010
 Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly
 320 325 330

cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa 1058
 Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu
 335 340 345

cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca 1106
 Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala
 350 355 360

aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att 1154
 Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile
 365 370 375 380

gtt att ctt tcg ctc gtt aga acc ggt tgatcgtgtt ataacatatg 1201
 Val Ile Leu Ser Leu Val Arg Thr Gly
 385

ccaatataca tgtctttggg cctacaatga catgatttgg tagttttcta atcaagcata 1261

tgtaatatataa tttgcttcga gaataaaata ataaaataaaa gtgtgatgtt acggtagacc 1321

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 35 40 45
 Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
 50 55 60
 Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
 65 70 75 80
 Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
 85 90 95
 Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
 100 105 110
 Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
 115 120 125
 Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
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 Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
 145 150 155 160
 Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
 165 170 175
 Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
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 Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
 195 200 205
 Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
 210 215 220
 Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
 225 230 235 240
 Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
 245 250 255

Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
 260 265 270
 Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
 275 280 285
 Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
 290 295 300
 Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
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 Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
 325 330 335
 Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
 340 345 350
 Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
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 <212> DNA
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<220>
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 <212> DNA
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<220>
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<210> 6
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<212> PRT

<213> Clarkia breweri

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Lys Pro Ile Thr Glu Ala Ala Ile Thr Ala Leu Tyr Ser Gly Asp Thr
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Val Thr Thr Arg Leu Ala Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
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Asn Ala Leu Phe Ala Val Thr Glu Leu Ile Lys Thr Val Glu Glu Leu
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Arg Lys Lys Met Gly Arg Glu Asn Ser Pro Glu Tyr Gln Ile Phe Leu
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Asn Asp Leu Pro Gly Asn Asp Phe Asn Ala Ile Phe Arg Ser Leu Pro
          100              105              110

Ile Glu Asn Asp Val Asp Gly Val Cys Phe Ile Asn Gly Val Pro Gly
 115              120              125

Ser Phe Tyr Gly Arg Leu Phe Pro Arg Asn Thr Leu His Phe Ile His
 130              135              140

Ser Ser Tyr Ser Leu Met Trp Leu Ser Gln Val Pro Ile Gly Ile Glu
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Ser Asn Lys Gly Asn Ile Tyr Met Ala Asn Thr Cys Pro Gln Ser Val
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Leu Asn Ala Tyr Tyr Lys Gln Phe Gln Glu Asp His Ala Leu Phe Leu
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Arg Cys Arg Ala Gln Glu Val Val Pro Gly Gly Arg Met Val Leu Thr
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 210              215              220

Ile Trp Gln Leu Leu Ala Met Ala Leu Asn Gln Met Val Ser Glu Gly
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Leu Ile Glu Glu Glu Lys Met Asp Lys Phe Asn Ile Pro Gln Tyr Thr
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Pro Ser Pro Thr Glu Val Glu Ala Glu Ile Leu Lys Glu Gly Ser Phe
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Leu Ile Asp His Ile Glu Ala Ser Glu Ile Tyr Trp Ser Ser Cys Thr
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7

Lys Asp Gly Asp Gly Gly Gly Ser Val Glu Glu Glu Gly Tyr Asn Val
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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